OM protein - protein search, using sw model

GenCore version 5.1.3
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Run on: November 30, 2002, 12:23:18 ; Search time 57.9734 Seconds
                                            (without alignments)
                                            3273.388 Million cell updates/sec

Sequence: 1 MAWLRLQPLTSAFLHFGLVT.........LWLLYILFATLEAYCYIKGF 921

Perfect_score: 4797
US-10-054-680-2

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Scoring table: BLOSUM62

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_21:*
               1: sp_archea:*
               2: sp_bacteria:*
               3: sp_fungi:*
               4: sp_human:*
               5: sp_invertebrate:*
               6: sp_mammal:*
               7: sp_mhc:*
               8: sp_organelle:*
               9: sp_phage:*
              10: sp_plant:*
              11: sp_rodent:*
              12: sp_virus:*
              13: sp_vertebrate:*
              14: sp_unclassified:*
              15: sp_rvirus:*
              16: sp_bacteriap:*
              17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4768.5	99.4	924	4	Q96QG1	Q96qg1 homo sapien
2	4671	97.4	925	4	Q96QG2	Q96qg2 homo sapien
3	4563.5	95.1	928	11	Q8VHJ8	Q8vhj8 mus musculu
4	3458.5	72.1	934	6	O97801	O97801 macaca mula
5	3442.5	71.8	941	6	Q28662	Q28662 oryctolagus
6	3437.5	71.7	941	6	Q9TS14	Q9ts14 oryctolagus
7	3427.5	71.5	934	11	Q9R238	Q9r238 rattus norv
8	3425.5	71.4	934	11	Q9WD30	Q9wd30 rattus norv
9	3417	71.2	957	11	Q9R239	Q9r239 rattus norv
10	3409.5	71.2	962	11	Q924Y2	Q924y2 rattus norv
11	3406	71.0	969	11	Q9WU29	Q9wu29 rattus norv
12	3290.5	68.6	968	13	Q9PT19	Q9pt19 oncorhynchu
13	3191.5	66.5	940	11	Q35157	Q35157 mus musculu
14	3012	62.8	595	11	Q9PPU8	Q9ppu8 mus musculu
15	2553	52.8	892	5	O02196	O02196 loligo opal
16	2203.5	45.9	925	5	O45630	O45630 caenorhabdi

17	2160.5	45.0	793	4	Q9H021	Q9h021 homo sapien
18	2156.5	45.0	602	6	Q9TV05	Q9tv05 macaca mula
19	2130.5	44.4	950	5	Q24413	Q24413 drosophila
20	2130.5	44.4	950	5	Q9VDG5	Q9vdg5 drosophila
21	2128.5	44.4	950	11	Q912J7	Q912j7 mus musculu
22	2126.5	44.3	600	11	Q9ET74	Q9et74 mus musculu
23	2119	44.2	950	5	O18367	O18367 drosophila
24	2102	43.8	583	13	Q91850	Q91850 xenopus lae
25	2096	43.7	955	13	Q94161	Q94161 caenorhabdi
26	2001.5	41.7	880	13	Q21609	Q21609 caenorhabdi
27	1912.5	39.9	560	11	Q91849	Q91849 xenopus lae
28	1278	26.6	254	13	Q9YH83	Q9yh83 gallus gall
29	1192	24.8	807	5	O21895	O21895 caenorhabdi
30	1105.5	23.0	263	5	Q9YGE0	Q9yge0 oncorhynchu
31	1046.5	21.8	263	13	Q9YH84	Q9yh84 gallus gall
32	1038	21.6	264	13	Q9YGE1	Q9yge1 oncorhynchu
33	970.5	20.2	267	13	Q9YGE2	Q9yge2 oncorhynchu
34	660	13.8	199	11	Q8R505	Q8r505 mus musculu
35	614.5	12.8	215	11	Q8R505	Q8r505 mus musculu
36	599.5	12.5	263	5	Q9Z0T8	Q9z0t8 rattus norv
37	579	12.1	539	10	Q8WPE2	Q8wpe2 porcellio s
38	573	11.9	133	11	O22252	O22252 arabidopsis
39	523.5	10.9	171	11	Q9Q49	Q9q49 rattus sp.
40	487	10.2	158	6	Q8R504	Q8r504 rattus sp.
41	481	10.0	92	11	Q9MYS4	Q9mys4 oryctolagus
42	424	8.8	92	6	Q8R503	Q8r503 mus musculu
43	329	6.9	107	6	Q91ZQ6	Q91zq6 mus musculu
44	318	6.6	1130	11	O97792	O97792 bos taurus
45	308	6.4	140	11	O91WD8	O91wd8 mus musculu
					Q62614	Q62614 rattus norv

ALIGNMENTS

RESULT 1
Q96QG1

ID   Q96QG1;   PRELIMINARY;   PRT;   924 AA.
AC   Q96QG1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Sodium/calcium exchanger SCL8A3.
GN   SCL8A3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gabellini N.;
RT   "Characterization of the human SCL8A3 gene for solute carrier family
RT   8, member 3 (sodium/calcium exchanger).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Bortoluzzi S.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ304853; CAC40985.1; -.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR004837; NaCa_Exchng.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
SQ   SEQUENCE 924 AA; 102694 MW; A0A556B753998A07 CRC64;

Query Match   99.4%; Score 4768.5; DB 4; Length 924;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches   918; Conservative   1; Mismatches   2; Indels   3; Gaps   1;

Qy   1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGSGDVPSTGQNNESCSGSSSDCKEGVIL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGSGDVPSTGQNNESCSGSSSDCKEGVIL 60

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Qy    61 PIWYPENPSLGDKIARVIYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 PIWPENPSLGDKIARVIYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy   121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy   181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy   241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy   301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360

Qy   361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy   421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480

Qy   481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy   541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDEDTYGELEFKNDETVKTIRV 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDEDTYGELEFKNDETVKTIRV 600

Qy   601 KIVDEEEYERQENFFIALGEPKWMERGISDV----TDRKLTMEEEEAKRIAEMGKPVLGEH 657
         |||||||||||||||||||||||||||    :||||||||||||||||||||||||||||
Db   601 KIVDEEAYEKNKNYFIEMVGPRMVDMSFQKALLLSPDRKLTMEEEEAKRIAEMGKPVLGE 660

Qy   658 PKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEATVSAAGDEDEDESGEER 717
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 PKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEATVSAAGDEDEDESGEE 720

Qy   718 LPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTI 777
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 LPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTI 780

Qy   778 GLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA 837
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA 840

Qy   838 AIYWALQQGEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRPHLGGELGGPRGCKLATTW 897
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 AIYWALQQGEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRPHLGGELGGPRGCKLATTW 900

Qy   898 LFVSLWLLYILFATLEACYIKGF 921
         |||||||||||||||||||||||
Db   901 LFVSLWLLYILFATLEACYIKGF 924
```

RESULT 2
Q96G2

ID   Q96G2   PRELIMINARY;   PRT;   925 AA.
AC   Q96G2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Sodium/calcium exchanger SCL8A3.
GN   SCL8A3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bortoluzzi S.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Gabellini N.;
RT   "Characterization of the human SCL8A3 gene for solute carrier family
RT   8, member 3 (sodium/calcium exchanger).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ304852; CAC40984.1; -.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR004837; NaCa_Exmemb.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
SQ   SEQUENCE   925 AA; 102803 MW; 0CCF8DA0881C4FDA CRC64;

Query Match   97.4%; Score 4671; DB 4; Length 925;
Best Local Similarity   96.9%; Pred. No. 0;
Matches 896; Conservative 11; Mismatches 14; Indels 4; Gaps 1;

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Qy     1 MAWLRLQPLISAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSSDCKEGVIL 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MAWLRLQPLISAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSSDCKEGVIL 60

Qy    61 PIWYPENPSLGDKIARVIYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 PIWPENPSLGDKIARVIYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy   121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy   181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy   241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy   301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360

Qy   361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy   421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480

Qy   481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy   541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDEDTYGELEFKNDETVKTIHI 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| :
Db   541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDEDTYGELEFKNDETVKTIRV 600

Qy   601 KIVDDEAYEKNKNYFIEMVGPRMVDMSFQKALLLSPDRKLTMEEEEAKRIAEMGKPVLGE 660
         |||| ||| : | ||: :||| ::      |||||||||||||||||||||||||||||
Db   601 KIVDEEEYERQENFFIALGEPKWMERGISDV----TDRKLTMEEEEAKRIAEMGKPVLGE 656

Qy   657 HPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEATVSAAGDEDEDESGEE 716
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   657 HPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEATVSAAGDEDEDESGEE 716

Qy   661 HPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEATVSAAGDEDEDESGEE 720
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Qy   717  RLPSCPFDYVWHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT  776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  RLPSCPFDYVWHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT  780

Qy   777  IGLKDSVTAVVFVARGTSVPDTFASKAAALQDVYADASIGNVTGSNAVVNVFLGIGLAWSV  836
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  IGLKDSVTAVVFVARGTSVPDTFASKAAALQDVYADASIGNVTGSNAVVNVFLGIGLAWSV  840

Qy   837  AAIYAWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT  896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  AAIYAWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT  900

Qy   897  WLFVSLWLLYILFATLEAYCYIKGF  921
          |||||||||||||||||||||||||
Db   901  WLFVSLWLLYILFATLEAYCYIKGF  925
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RESULT 3

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ID   Q8VHJ8      PRELIMINARY;      PRT;     928 AA.
AC   Q8VHJ8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Sodium/calcium exchanger.
GN   SLC8A3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SKELETAL MUSCLE;
RA   Kraev A.;
RT   "Towards complete inventory of calcium transporters of the house
RT   mouse.";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF453257; AAL39160.1; -.
DR   MGD; MGI:107976; Slc8a3.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR004837; NaCa_Exmemb.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   PRINTS; PR01259; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 1.
DR   TIGRFAMS; TIGR00845; caca; 1.
SQ   SEQUENCE   928 AA;  102943 MW;  A36BBB30EE4123C0 CRC64;
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Query Match   95.1%;
Best Local Similarity   94.2%;
Matches 874;   Conservative 21;   Mismatches 26;   Indels 7;   Gaps 1;
Score 4563.5;   DB 11;   Length 928;   Pred. No. 0;

```
Qy     1  MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSGSSDCKEGVIL  60
          |||||||||||||||||||||||||||.||||||.||||||.|||.||||||||   ||||||
Db     1  MAWLRLQPLTSAFLHFGLVTFVLFLNCLRAEAGDSGDVPSAGQNESCSGSSDCKEGVIL  60

Qy    61  PIWPENPSLGDKIARVIVFVALIMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  PIWPENPSLGDKIARVIVFVALIMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE  120

Qy   121  TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI  180

Qy   181  IIGICVYVIPDGETRKIKHLRVFFIIAAWSIFAYIWLYMILAVFSPGVQVQWEGLLTLFF  240
          ||||||||||||||||||||||||||.||||||||||||||||||||||||||||||||||
Db   181  IIGICVYVIPDGETRKIKHLRVFFVIAAWSIFAYIWLYMILAVFSPGVVQVQWEGLLTLFF  240

Qy   241  FPVCVLLAWVADKRLLFYKXMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  FPVCVLLAWVADKRLLFYKXMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN  300
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Qy   301  LYPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR  360
          |.|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  FTFLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR  360

Qy   361  MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLTVVR  420
          |||||||||||.||||||.||||||||||||||||.||||||||||||||||||||||||
Db   361  MMTGAGNILKIKHAAEQAKKTSSMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLTVVR  420

Qy   421  KGDMSKTMYDYKTEDGSANAGADYEFTEGTVWLKPGETQKEFSVGIIDDIFEEDEHF  480
          ||.|.||||.||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  KGGDISKTMYVDYKTEDGSANAGADYEFTEGTVWLKPGETQKEFSVGIIDDIFEEDEHF  480

Qy   481  FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH  540
          |||||||||.|||.|.||.||||.|||||||||||||||||||||||||||||||||||||
Db   481  FVRLSNVRVEEEQLAEGMLPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH  540

Qy   541  VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKITRV  600
          |||||||||||||||||||||||||||||||||||||||||.||||||||||||||.::.
Db   541  VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDAYGELEFKNDETVKTIHI  600

Qy   601  KIVDEEEYERQENFFIALGEPKMWERGIS------------DVTDRKLTMEEEEAKRIAEMGKPV  653
          |::||..:...::.:::.|.|.:.::.:.|:          ::|||||||.|||||||||||||
Db   601  KVIDDKAYEKNKNYVIEMMGPRNVDMSVQKALLLSPEVTDRKLTVEEEEAKRIAEMGKPV  660

Qy   654  LGEHPKLEVIIEESYERKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDES  713
          ||||||||||||||||||.||||||||||.|||||||||||||||||||||.||.||||||
Db   661  LGEHPKLEVIIEESYERKSTVDKLIKKTNIALVVGTHSWRDQFMEAITVSAGDGDEDES  720

Qy   714  GEERLPSCPFDYVWHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHF  773
          ||||||||||||||||||||||||||||||||||.|||||.|||||||||||||||||||||
Db   721  GEERLPSCPFDYVWHFLTVFWKVLFACVPPTEYCPGWACFVVSILIIGMLTAIIGDLASHF  780

Qy   774  GCTIGLKDSVTAVVFVARGTSVPDTFASKAAALQDVYADASIGNVTGSNAVVNVFLGIGLA  833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GCTIGLKDSVTAVVFVARGTSVPDTFASKAAALQDVYADASIGNVTGSNAVVNVFLGIGLA  840

Qy   834  WSVAAIYAWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKL  893
          |||||||||.|||||||||||||||||||||||||||.||||||||||||||||||||||||
Db   841  WSVAAIYAWAMQGQEFHVSAGTLAFSVTLFTIFAFVCLSVLLYRRRPHLGGELGGPRGCKL  900

Qy   894  ATTWLFVSLWLLYILFATLEAYCYIKGF  921
          ||||||||||||||||||||||||||||
Db   901  ATTWLFVSLWLLYILFATLEAYCYIKGF  928
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RESULT 4

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ID   O97801      PRELIMINARY;      PRT;     934 AA.
AC   O97801;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Sodium-calcium exchanger isoform NCX1.3.
GN   NCX1.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE=99175198; PubMed=10075718;
RA   Li X.F., Lytton J.;
RT   "A circularized sodium-calcium exchanger exon 2 transcript.";
RL   J. Biol. Chem. 274:8153-8160(1999).
DR   EMBL; AF107593; AAD04173.1; -.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR004837; NaCa_Exmemb.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
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DR   PRINTS; PR01259; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
SQ   SEQUENCE   934 AA; 104331 MW; 2A22BDA30254BBC2 CRC64;

Query Match   72.1%; Score 3458.5; DB 6; Length 934;
Best Local Similarity   71.8%; Pred. No. 3.1e-244;
Matches 676; Conservative 108; Mismatches 129; Indels   29; Gaps 10;

Qy   1 MAWLRLQPLTSAFLHFGLVTEVLF--LNGLRAEAGGSGDVPSTGQNNESCSGSSSDCKEGV 58
          |||| | : || :| ||| | : || ||| |||| || : |||||||||||||||
Db   1 MRRLSLSFPTFSMGFHLLVIVALLFFHVDYIVIATEMEGGNETGE----CTGSYYCKKGV 56

Qy   59 ILPIWYPENPSLGDKIARVIVFVALIYMFLGVSIIIADRFMASIEVITSQEREVTIKKPN 118
          |||| | |||||||||||||||| ||| ||||||||||||||||||||| ::||| ||
Db   57 ILPIWEPQDPSFGDKIARATVFVFVAMVYMFLGVSIIIADRFMSSIEVITSQEKEITIKKPN 116

Qy   119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178
          ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176

Qy   179 FIIIGICVYVIPDGETRKIKHLRVFFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238
          ||||| |||||||||||||||||||| | || ::|||||: ||||||||||||||||||||
Db   177 FIIIALCVYVVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 236

Qy   239 FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 295
          ||||| ||||||| |||||||||||:|||||||||||||||||||| |||||||||:|
Db   237 FFFPICVVPAWVADRRLLFYKIVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSH 296

Qy   296 ---FLDGNIVPLEGKEVD---------ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   297 VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy   349 KSRAFYRIQATRMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
          |||||||||||||||||||||||:||| | :|| ||||||||| :||||||||| :|||
Db   356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYQC 415

Qy   408 LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
          ||||| |||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   416 LENCGTVALTIIRRGGDLTNTVVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy   468 IIDDDIFEEDENFLVHLSNVKVSSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 527
          |||||||||||| | :||: | | : |||| :: | ||||| || |: ||||||
Db   476 IIDDDIFEEDEHFFVRLSNVRIEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527

Qy   528 HAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYCEL 587
          |||||| |||||| | ::|| ||| || :| ||| | | ||| |||||||||||||||
Db   528 HAGIFTFEEPVTHVSESIGIMEVKVLRISGARGNVIVPYKTIEGTARGGGEDEDTCGEL 587

Qy   588 EFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG------ISDVTDRK--LTME 639
          :|||:||||||||:|||||:| ::|||| |||| || ||||| | |: |
Db   588 DPSFGDKIARATVFVFVAMVYMFLGVSIIADRFMSSIEVITSPGIVEVWEGLLTFFFFPICVV 639

Qy   640 EEEAKRIAEMGKPVLGEHPKLEVIEESYEFKTTVDKLIKKTNLALVVGTHSNRDQEMEA 699
          || | ||| | |||| | ||||||| |: |:| |||| ||| |:||| : |||:|||
Db   640 EFQNDEIVKIIITRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTIDEYDKQPLISK 652

Qy   700 ITVSAAGDEDEDSGEERLPSCFDYVMHFLTVEWKVLFACVPPTEYCHGWACFAVSLILI 759
          |||| | |:||:|| ||| || ||| ||| |: | | ||| | | || |::|:|:|
Db   653 EEEERRIAEMGRPILGEHTKLEVIEESYEFKSTVDKLIKKINLALVGTNSWREQFIEA 712

Qy   713 ITVSAGEDDDDDECGEERKLPSCFDYVMHFLTVFWKVLPAFVPPTEYWNGWACFIVSILMI 772
          |||| | |||||| |||:|||| ||| || :||||| ||||| || ||||| |:|:| |
Db   713 RVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICV 772

Qy   773 GLLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKAAALQDVYADASIGNVT 832
          |||| ||||||:|||| |||||| | |:| | |: |||| || ::| ||| || |||:|
Db   773 RIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIIALCV 832

Qy   833 GSNAVNVFLGIGLAWSIAAIYHAANGEQFKVSPGTLAFSVTLFTIFAFVCISVLLYRRP 892
          |||| ||||| ||||| || ||:|||:||||||||||||||||| ||:|| ||||||:|
Db   833 GMLTAIIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKAAALQDVYADASIGNVT 892

Qy   880 HLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
          : ||||| | : : | || || |: | |||||||||||||||
Db   893 EIGGELGGPRTAKLLTSCLFVLLMLLYIFFSSLEAYCHIKGF 934

RESULT 5

ID   Q28662   PRELIMINARY;   PRT;   941 AA.
AC   Q28662;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Renal Na/Ca exchanger NACA-2.
GN   NCX1.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE=92321271; PubMed=1621815;
RA   Reilly R.F., Shugrue C.A.;
RT   "cDNA cloning of a renal Na(+)-Ca2+ exchanger.";
RL   Am. J. Physiol. 262:F1105-F1109(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Reilly R.F., Shugrue C.A.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RL   EMBL; U52665; AAA97928.1; -.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR004837; Na_Ca_Exmemb.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   PRINTS; PR01259; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
SQ   SEQUENCE   941 AA; 105128 MW; 7E1139EDE70A4084 CRC64;

Query Match   71.8%; Score 3442.5; DB 6; Length 941;
Best Local Similarity   71.8%; Pred. No. 4.7e-243;
Matches 669; Conservative 109; Mismatches 128; Indels   35; Gaps 10;

Qy   8 PLTSAFLHFGLVTEVLF-LNGLRAEAGGSGDVPSTGQNNESCSGSSSDCKEGVILPIWYPE 66
          || || ||||||| : | |||||||||||||||||||||||||||||||||||||||||
Db   9 PFSMGFHLLAIVALFFFRVDHVSAETEMEGGNETGE----CTGSYYCKKGVILPIWEPQ 64

Qy   67 NPSLGDKIARVIVFVALIYMFLGVSIIIADRFMASIEVITSQEREVTIKKPNGETSTTTI 126
          |||||||||||||||| ||||||||||||||||||||||||||| ::||| ||| |:
Db   65 DPSFGDKIARATVFVFVAMVYMFLGVSIIADRFMSSIEVITSPGIVEVWEGLLTFFFFPICVV 124

Qy   127 RVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICV 186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   125 RIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIIALCV 184

Qy   187 YVIPDGETRKIKHLRVFFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVL 246
          |||||||||||||||| | || :|||||:||||||||||||||:|||||||:|||||:|
Db   185 YVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTFFFFPICVV 244

Qy   247 LAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 304
          ||| ||||||||||:|||:|||||||||||||||||||| |||||||||:|
Db   245 FAWVADRRLLFYKIVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSH 304

Qy   301 LVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRI 356
          || |||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   305 LV-LDVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRAFYRI 363

Qy   357 QATRMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCGAVL 415
          |||||||||||||||:||| | :|| |||||||||| :||||||||| :|||||||| |
Db   364 QATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYQCLENCGTVA 423

Qy   416 LTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFE 475
          ||| |||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   416 LTIIRRGGDLTNTVVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVGIIDDDIFE 475

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RESULT 6
Q9TS14

ID   Q9TS14       PRELIMINARY;      PRT;   941 AA.
AC   Q9TS14;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   NA/CA exchanger isoform NACA6.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94148976; PubMed=8106495;
RA   Kofuji P., Lederer W.J., Schulze D.H.;
RT   "Mutually exclusive and cassette exons underlie alternatively spliced
RT   isoforms of the Na/Ca exchanger.";
RL   J. Biol. Chem. 269:5145-5149(1994).
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR001123; DnaJ_N.
DR   InterPro; IPR004836; NaCa_Exmemb.
DR   InterPro; IPR004837; NaCa_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_ex; 2.
DR   PRINTS; PR01259; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00045; caca; 1.
DR   PROSITE; PS50076; DNA_2; 1.
SQ   SEQUENCE  941 AA;  104995 MW;  AEC76774E99B81815 CRC64;


Query Match             71.8%;
Best Local Similarity   71.0%;
Matches  669;  Conservative 111;  Mismatches 125;  Indels 37;  Gaps 11;
Score 3437.5;  DB 6;  Length 941;  Pred. No. 1.1e-242;
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Qy     8  PLTSAFLHFGLVTFVLF-LNGLRAEAGSGDVPSTGONNESCGSGSSDCKEGVTLPIWYPE   66
          |::|| |  :||| ::|  |:||  |  | ||  |::  ||  ::|:|  :|:||| |:
Db     9  PFSMGFHLLAIVALFFFRVDHVSAETEMEGEGNETGE----CIGSYCKKGVILPIWPQ    64

Qy    67  NPSLGDKIARVIVYFVALLYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETTTTTI  126
Db    65  DPSFGDKIARATVFVAAMYMFLGVSIIADRFMSSIEVITSQEKEITIKK-NGETTKTTV   123

Qy   127  RVWNETVSNLTLMALGSSAPEILLSIIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICV  186
Db   124  RIWNETVSNLTLMALGSSAPEILLSVIEVCGHNETAGDLGPSTIVGSAAFNMFIIIALCV  183

Qy   187  YVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGCVVQVWEGLLTLFFPPVCVL  246
Db   184  YVVPDGETRKIKIHLRVFFVTAAWSIFAYTWLYIILSVISPGIVEVWEGLLTFFFFPICVV  243

Qy   247  LAWWADKRLLFYKYMHKKYRTDKIRGIIIIIETEGDHPKG----IEMDGKMMNSH---FLDGN  300
Db   244  FAWWADRRLLFYKYVYKIRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVNSHVDNFLDGA    303

Qy   301  LVPLEGKEVD-----ESRREMIRILKDLKOKHPEKDLDQLVEMANYYALSHQQKSRAFYRI  356
Db   304  LV-LDVDERQODDEEARREMARILKELKQKHPEKEIEOLLELANYQVLSQOQKSRAFYRI    362

Qy   357  QATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYCLENCGAVL    415
Db   363  QATRLMTGAGNILKRHAADQOARKAVSMHEVVNTEMAENDPVSKIFFEOQGTYQCLENCGTVA  422

Qy   416  LTVVRKGGDMSKTMTVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEPSVGIIDDDIFE  475
Db   423  LIIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVGIIDDDIFE  482

Qy   476  EDEHFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTE    535
Db   483  EDENFLVHLSNVKVSSETSEDGILEANHIS---TLACLGSPCTATVTIFDDDHAGIFTE   539

Qy   536  CDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDDTYGELEFKNDETV 595
Db   540  ESVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGELEFQNDEIV  599

Qy   596  KTIRVKIVDEEYERQENFFIALGEPKWMERG----------------ISDVTDRK--LTMEE 639
Db   600  KTISVKIVDDEEYERKNKTFFLEIGEPRLVEMSERKKALLLNELGGFTITEEYDDKQPLTSK 659

Qy   640  EEEAKIRIAEMGKPVLGEHPKLEVIIEESYEKFKTTVDKLIKKTNLALVVGTHSWRDQFMEA 699
Db   660  EEERRIAEMGRPILGEHTKLEVIIEESYEKFKSTVDKLIKKTNLALVVGTNSWREQFIEA   719

Qy   700  ITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILLI  759
Db   720  ITVSAGEDDDDECGEEKLPSCFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMI   779

Qy   760  GMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVT  819
Db   780  GLITAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATQDQYADASIGNVT  839

Qy   820  GSNAVNVFLGIGLAWSVAAIYWALQGEEFHVSAGTLAFSVTLFTIFAFVCISLVLLYRRP  879
Db   840  GSNAVNVFLGIGVAWSIAAIYHAANGEHFKVSPGTLAFSVTLFTIFAFINVGVLLYRRP   899

Qy   880  HLGGELGGPRGCKLAITTWLFVSLMLLYILFATLEAYCYIKGF  921
Db   900  EIGGELGGPRTAKLLTSCLFVLLMLLYIFFSSLEAYCHIKGF   941
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RESULT 7
Q9R238

ID   Q9R238       PRELIMINARY;      PRT;   934 AA.
AC   Q9R238;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Na+/Ca2+-exchanging protein.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   STRAIN=DAHL/Rapp R SPRAGUE-DAWLEY;
RC
RT   "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT   Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
     EMBL; AF109163; AAD23386.1;
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   InterPro; IPR004837; NaCa_Exmemb.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   PRINTS; PR01259; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
SQ   SEQUENCE   934 AA;   104166 MW;   C04E0D8A75633DDC CRC64;

Query Match    71.5%;   Score 3427.5;   DB 11;   Length 934;
Best Local Similarity   70.9%;
Matches  671;  Conservative  107;  Pred. No. 5.8e-242;  Mismatches  127;  Indels  41;  Gaps  11;

Qy    4  LRLQPLTSAFLHFGLVTFVLFL-------NGLRAEAGGSGDVPSTGQNNESCSGSSDCK  55
            ||| :||||||:|:| ::|||       :||||||||||||| | ||||  ||||
Db    2  LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGN--------ETTECTGSYCK  53

Qy   56  EGVILPIWPENPSLGDKIARVIVFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK  115
            |||:||||| | |||||||||:||||||:|||||||||||||||||||||||||||||
Db   54  KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADREMSSIEVITSQEKEITIK  113

Qy  116  KPNGETSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFPIAGDLGPSTIVGSAA  175
            ||||||| |||||||||||||||||||||||||||||||:||||  | ||||||||||
Db  114  KPNGETTKTIVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA  173

Qy  176  FNMFIIIGICVYVIPDGETRKIKLHLRVFEITAAWSIFAYIWLYMILAVPSPGVVQVWEGL  235
            |||||||||||| |||||||||| ||||||:||| ||||||||||:|||||:|||||||||
Db  174  FNMFIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL  233

Qy  236  LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIIETEGDHPKG---IEMDGKMM  292
            ||:|||||||:|||| ||||||||||||||||||||:||:||||||||||   ||||||||
Db  234  LTFFFFPICVFAWVADRLLFYKVYKRYRAGKQRGMIIEHEGDRPASKTEIEMDGKVV  293

Qy  293  NSH----FLDGNLVPLEGKEVD------ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS  345
            |:|    ||| ||  :|||:||       :||:|:  |||||| |: ::||:||||||| |||
Db  294  NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS  352

Qy  346  HQQKSRAFYRIQATRMMYGAGNLKKHAAEQAKRASSMSEVHTDEPE-DFISKVFFDPCS  404
            |||||||||||| |||| |||||||:| |:|| |:|||  |:||| |||||||:||
Db  353  QQQKSRAFYRIQATRLMTGAGNLIKRHAADQARKAVSMHEVNMDVVENDDVSKVFFEQGT  412

Qy  405  YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSSANAGADYEFTEGTIVVLKPGETQKEF  464
            |||||:|| |||||:|:|||:|||||||| | | |||||| ||| ||||| |||||||||
Db  413  YQCLENCGVALIIRRGGDLTNVSVDEYPERDGTANAGSDYEFTEGTIVFKPGETQKEI  472

Qy  465  SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIPNSLPLPR-AVLASPCVATVTI  523
            ||||||||||||||  |:||| || ||| ||||| ||| |: ||   ::|||:|||:|
Db  473  RVGIIDDDIFEEDENFLVHLSNVRSSSEVSEDG-----ILDSNHVSAIACLGSPNTATITI  528

Qy  524  LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPRTVEGTAKGGGEDFEDT  583
            ||||||||| ||| ||||||| |||| :||||| |  ||| | | | | | || ||||
Db  529  FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTPARGGGEDFEDT  588

Qy  584  YGELEFKNDETVKIRVKIVDEEEYERQENFFIALGEPKWMERGI-------SDVTDRK-  635
            |||||||:|| ||||| ||:||| ::|| ||||||| |:|||         ||:|||
Db  589  CGELEFQNDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRGCMKGGFTLTEEYDDKQP  648

Qy  636  LTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESVEFKTVVDKLIKKTNLALVVGTHSWRDQ  695
            |||||||| |:||||  ||||| |||||||| ||| :||||:|||||:||:|||:|| :|
Db  649  LTSKEEERRIAEMGRPILGEHKLEVIIEESYEFKSTVDKLIKKKTNLALVVGTHNSWREQ  708
```

```
Qy  696  FMEAITVSAAGDEDEDESGEERLPSCFDYWHFLTVFWKVLFACYPPTEYCHGWACFAVS  755
            |:||||||| ||:|:| |||::|||| |||  |||||||||  || |||: || |||| |
Db  709  FIEAITVSAGEDDDDDECGEEKLPSCGFDYVWHFLTVFWKVLPFAFVPPTEYWNGWACFIVS  768

Qy  756  ILIIGMLTAIIGDLASHFGCTIGILKDSVTAVVFAVEAFGTSVPDTFASKAAALQDYADASI  815
            ||:||:|||:|||||||||||||||||||||||||| | ||||||||||||||| |||||||
Db  769  ILMIGLLTAFIGDLASHFGCTIGILKDSVTAVVFAVLGTSVPDTFASKVAARQODQYADASI  828

Qy  816  GNVTGSNAVNVFLGIGLAWSVAAIVWALQGQEFHVSAGTLAFSVLFTIFAFVCISVLLY  875
            |||||||||||||||| |||:|||| |  |:||:||||||||||||||||||:  |||
Db  829  GNVTGSNAVNVFLGIGVAWSIAAIVHAANGEQFKVSPGTLAFSVLFTIFAFINGVLLY  888

Qy  876  RRRPHLGGELGGPRGCKLATTWLFVSLLWLLYILFATLEAYCIKGF  921
            |||| :||||||||  |:| |:| ||:||||||:||:|||||  |||
Db  889  RRRPEIGGELGGPRTAKLLTGSSLFVLLWLLYIFFSSLEAYCHIKGF  934
```

RESULT 8
Q9WU30

```
ID   Q9WU30        PRELIMINARY;       PRT;   934 AA.
AC   Q9WU30;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-2002 (TrEMBLrel. 21, Last annotation update)
DE   Na+/Ca2+-exchanging protein.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Unlap M.T., Bell P.D.;
RC   STRAIN=SPRAGUE-DAWLEY;
RT   "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT   Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
     EMBL; AF109166; AAD23389.1;
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   InterPro; IPR004837; NaCa_Exmemb.
DR   Pfam; PF03160; Calx_beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   PRINTS; PR01259; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
SQ   SEQUENCE   934 AA;   054D06E9179098B5 CRC64;

Query Match    71.4%;   Score 3425.5;   DB 11;   Length 934;
Best Local Similarity   70.8%;
Matches  670;  Conservative 108;  Pred. No. 8.2e-242;  Mismatches  127;  Indels  41;  Gaps  11;

Qy    4  LRLQPLTSAFLHFGLVTFVLFL-------NGLRAEAGGSGDVPSTGQNNESCSGSSDCK  55
            ||| :||||||:|:| ::|||       :||||||||||||| | ||||  ||||
Db    2  LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGN--------ETTECTGSYCK  53

Qy   56  EGVILPIWPENPSLGDKIARVIVFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK  115
            |||:||||| | |||||||||:||||||:|||||||||||||||||||||||||||||
Db   54  KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADREMSSIEVITSQEKEITIK  113

Qy  116  KPNGETSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFPIAGDLGPSTIVGSAA  175
            ||||||| |||||||||||||||||||||||||||||||:||||  | ||||||||||
Db  114  KPNGETTKTIVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA  173

Qy  176  FNMFIIIGICVYVIPDGETRKIKLHLRVFEITAAWSIFAYIWLYMILAVPSPGVVQVWEGL  235
            |||||||||||| |||||||||| ||||||:||| ||||||||||:|||||:|||||||||
Db  174  FNMFIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL  233

Qy  236  LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIIETEGDHPKG---IEMDGKMM  292
            ||:|||||||:|||| ||||||||||||||||||||:||:||||||||||   ||||||||
Db  234  LTFFFFPICVFAWVADRLLFYKVYKRYRAGKQRGMIIEHEGDRPASKTEIEMDGKVV  293
```

```
RESULT 9
Q9R239

ID   Q9R239;      PRELIMINARY;   PRT;   957 AA.
AC   Q9R239;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Na+/Ca2+-exchanging protein.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DAHL/RAPP S SPRAGUE-DAWLEY;
RA   Unlap M.T., Bell P.D.;
RT   "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT   Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL   Submitted (NOV-1998) to the EMBL/Genbank/DDBJ databases.
DR   EMBL; AF109164; AAD23387.1; -.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR004837; NaCa_Exmemb.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   PRINTS; PR01259; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
SQ   SEQUENCE   957 AA;  106724 MW;  7A146330451EAA7E CRC64;
```

```
Query Match             71.2%;  Score 3417;  DB 11;  Length 957;
Best Local Similarity   69.5%;  Pred. No. 3.5e-241;
Matches  673;  Conservative 104;  Mismatches 128;  Indels 64;  Gaps 11;
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Qy      293 NSH----FLDGNLVPLEGKEVD-------ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS 345
                |||       |||:|||||||             :||||||||||||||||||:|::||||||:|||
Db      294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352

Qy      346 HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
                |||||||||||||||:||||||||||||::|||||||:|||||:|||||   ||||||||||||||
Db      353 QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412

Qy      405 YQCLENCGAVLLTVVRKGGDMSKTMVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
                |||||||||||:||||||:||       ::|||||::||||:|||||||||||||||||||||||
Db      413 YQCLENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472

Qy      465 SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
                |:|||||||||||||||||||||||     :|||||||||||||||||||||||| ||   ||:||
Db      473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528

Qy      524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPPRTVEGTAKGGGEDFEDT 583
                |||||||||||||:||||||||||||||||||||||||||||||||||||||||:||||||||||
Db      529 FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588

Qy      584 YGELEPKNDEIVKTIRVKIVDEEEYERQENFFIALGEPKWMERGI-------SDVTDRK- 635
                ||||||||:||||:|||||:||||||:||::|||||||:||||||      ::|:|||:
Db      589 CGELEFQNDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTEEYDKQP 648

Qy      636 LTMEEEEAKRIAEMGKRVLGEHPKLEVIIEESYEFKTVDKLIKKTNLALVVGTHSWRDQ 695
                ||:||||||||||||||:|||:||||||||||||:|::|||||||||||||:|||||||:|
Db      649 LTSKEEEERIAEMGRPILGEHTKLEVIIEESYEFKSTVDKLIKKINLALVVGTINSWREQ 708

Qy      696 FMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVS 755
                |:|||||||:|||||||:||||||||||||||||||:|||||:||:||||||:|||||:
Db      709 FIEAITVSAGEDDDDCGEEKLPSCFDYVMHFLTVFWKVLFAFVPPTEYNGWACFIVS 768

Qy      756 ILIIGMLTAIIGDLASHFPGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASI 815
                :||:||:||:|||||||||||||||||||||||||||||||||||||||::|||||||||||
Db      769 ILMIGLITAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATQDQYADASI 828

Qy      816 GNVTGSNAVNVFLGIGLAWSVAAIYWALQGGEFHVSAGTLAFSVLTFTIFAFVCISVLLY 875
                ||||||||||||||:|||||:||||:|||||||||||:||||||||||||||:|:|||||
Db      829 GNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQFKVSPGTLAFSVTLFTIFAFINVGVLLY 888

Qy      876 RRRPHLGGELGGPRGCKLATTWLFVSLWLLLYILFATLEAYCYIKGF 921
                |||:|||||||||:|||:||||||||||||||:|||||||||||||||
Db      889 RRRPEIGGELGGPRTAKLLTSSLFVLLMLLYIFFSSLEAYCHIKGF 934
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DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
SQ   SEQUENCE   957 AA;  106724 MW;  7A146330451EAA7E CRC64;

Query Match             71.2%;  Score 3417;  DB 11;  Length 957;
Best Local Similarity   69.5%;  Pred. No. 3.5e-241;
Matches  673;  Conservative 104;  Mismatches 128;  Indels 64;  Gaps 11;

Qy        4 LRLQPLTSAFLIHFGCLVTFVLFL-------NGLRAEAGGSGDVPSTGQNNESGSGSSDCK 55
                :||:|||||||||:|||||:||:|||           |:|:|||:||:|:|| :|||::|:|| ||
Db        2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEATEAETGGN------ETTECTGSYCK 53

Qy       56 EGVTLPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
                :||:|||||:|||||||||||:|||||||:|||||||||||||||||||:||||:||:|||||||
Db       54 KGVTLPIWEPQDPSFGDKIARATYVFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113

Qy      116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSIIEVCGHGFIAGDLGPSTIVGSAA 175
                |||||:|||||:||||||||:||||||||::|||||:|||||:||:|||||||||||||:||
Db      114 KPNGETTKTTVRINWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA 173

Qy      176 FNMFIIIGICVYLVIPDGETRKIKIHLRVFEITAAWSIFAYIWLYMILAYPSPGVVQVWEGL 235
                |||||||:|:|| ||||||:|||||||||:|||::||||||:||||:|:|:||||::|||:||
Db      174 ENMFIIIALCVYVVPDGETRKIKLHLRVFEVTAAWSIFAYLWLYIFLSVSSPGVVEWEGL 233

Qy      236 LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMM 292
                ||||||||||||||| :||:||||||:::||:|||:||:||||||||  ||           |:||||:||
Db      234 LTFFFFPICVFAWVADRLLFYKYVKRYRAGKORGMIIEHEGDRPASKTEIEMDGKVV 293

Qy      293 NSH----FLDGNLVPLEGKEVD-------ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS 345
                |||       |||:|||||||             :||||||||||||||||||:|::||||||:|||
Db      294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352

Qy      346 HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
                |||||||||||||||:||||||||||||::|||||||:|||||:|||||   ||||||||||||||
Db      353 QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412

Qy      405 YQCLENCGAVLLTVVRKGGDMSKTMVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
                |||||||||||:||||||:||       ::|||||::||||:|||||||||||||||||||||||
Db      413 YQCLENCGTVALTIIRRGGDLTNTVSVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472

Qy      465 SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
                |:|||||||||||||||||||||||     :|||||||||||||||||||||||| ||   ||:||
Db      473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528

Qy      524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPPRTVEGTAKGGGEDFEDT 583
                |||||||||||||:||||||||||||||||||||||||||||||||||||||||:||||||||||
Db      529 FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588

Qy      584 YGELEPKNDEIVKTIRVKIVDEEEYERQENFFIALGEPKWMERG-------SDVTDRK- 635
                ||||||||:||||:|||||:||||||:||::|||||||:|||||      ::|:|||:
Db      589 CGELEFQNDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTEEYDKQP 648

Qy      673 TVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGEDDDDCGEEKLPSCFDYVMHFLTVF 732
                ||||||||||||||:|||||||:|::||||||:||||||:|||||||||||||||||||||:
Db      649 HARDHPIPSTVISISEEYDKQPLTSKEEEERIAEMGRPILGEHTKLEVIIEESYEFKS 708

Qy      628 ---------ISDVTDRK--LTMEEEEAKRIAEMGKRVLGIGLAWSVAAIYWALQGGEFHVSA 672
                          :|:  ||||||   |||:||||||||||:||:       ::       |:::|
Db      589 CGELEFQNDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTEEYDKQP 648

Qy      733 WKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFPGCTIGLKDSVTAVVFVAFG 792
                ||||||:||:||||   |||||:||:||:||||:|||||||||||||||||||||||||| |
Db      769 WKVLFAFVPPTEYNGWACFIVSILMIGLITAFIGDLASHFGCTIGLKDSVTAVVFVALG 828

Qy      793 TSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGGEFHVSA 852
                ||||||||||::|||||||||||||||||||||||||:|||||:||||:|||||||||||:
Db      829 TSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQFKVSP 888

Qy      853 GTLAFSVLTFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLLYILFATL 912
                ||||||||||||||||:|:|||||||||:|||||||||:|||:|||||||||||||:|||||
Db      829 TSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQFKVSP 888

Qy      673 TVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGEDDDDCGEEKLPSCFDYVMHFLTVF 732
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Qy  913 EAYCYIKGF 921
        |||:|:|||
Db  949 EAYCHIKGF 957
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RESULT 10

```
ID   Q924Y2      PRELIMINARY;   PRT;   962 AA.
AC   Q924Y2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Na+/Ca2+ exchanger.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RA   Unlap M.T., Bell P.D., Williams I.;
RT   "Cloning and expression of a mesangial cell Na+/Ca2+ exchanger from
RT   Sprague-Dawley rats.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY033398; AAK52307.1; -.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR004837; NaCa_Exchmemb.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
SQ   SEQUENCE   962 AA;  107270 MW;  1AA422ED25964182 CRC64;

Query Match        71.1%;  Score 3409.5;  DB 11;  Length 962;
Best Local Similarity    69.0%;  Pred. No. 1.3e-240;
Matches  672;  Conservative  105;  Mismatches 128;  Indels  69;  Gaps  11;

Qy    4 LRLQPLTSAFLHFGLVTFVLFL-----------NGLRAEAGGSGDVPSTGQNNESCSGSSSDCK 55
         |||                               ||:||||||||||||||||||||||||||
Db    2 LRLSLPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN------------ETTECTGSYYCK 53

Qy   56 EGVLPIWPENPSLGDKIARVIVYFVALIYMFLGVSIIADREMASIEVITSQEREVTIK 115
Db   54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADREMSSIEVITSQEKEITIK 113

Qy  116 KPNGETSTTTIRVWNETVSNLILMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
Db  114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLPSVIEVCGHNFTAGDLGPSTIVGSAA 173

Qy  176 FNMFIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGL 235
Db  174 FNMFIIALCVVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233

Qy  236 LTLFFFPVCVLLAWVADKRLLFYKYMHKYRTDKHRGIIIIETEGDHPKG---IEMDGKMM 292
Db  234 LTFFFFPICVVFAWVADDRLLFYKYVVKRYRAGKQRGMIIEHEGDRPASKTEIEMDGKVV 293

Qy  293 NSH---FLDGNLVPLEGKEVD------ESRREMIRILKDLKQKHPEKDLDQLVEMANYIALS 345
Db  294 NSHVDNFLDGALV-LEVDERDQODDEEAREMARILKELKQKHPDKEIEOLIELANYQVLS 352

Qy  346 HQQKSRAFYRIQARTRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFEQT 404
Db  353 QQQKSRAFYRIQATRLMTGAGNLKRHAADQARKAVSMHEVANMDVVENDPVSKVFFEQCT 412

Qy  405 YCCLENCGAVLLIVVVRKGGDMSKTMVYDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
Db  413 YCCLENCGTVALIIIRGGDLINTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETOKEI 472

Qy  465 SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
Db  473 RVGIIDDDIFEEDENFLVHLSNVRVSSGVSEDG-----------ILDSNHVSAIACLGSPNTATITI 528

Qy  524 LDDDHAGIFFECDTIHVSEBSIGVMEVKVLRTSGARGTVIVPFRTVEGTPAKGGGEDFEDT 583
Db  529 FDDDHAGIFFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKIIEGTARGGGEDFEDT 588

Qy  584 YGELEFKNDETVKIIRVKIVDEEYEYRQRQENFFIALGEPKWMERG----------- 627
Db  589 CGELEFQNDEIVKIITTIRIFDREEYEKECSFSLVLEEPKWIRGMKGGFILTGKKMYGQP 648

Qy  628 ------------ISDVTDRK--LTMEEEAKRIAEMGKRPVLGEHPKLEVIIEES 667
Db  649 VFRKVHARDHPIPSTVISISEEYDDKQPLISKEEEERRIAEMGRPILGEHTKLEVIIEES 708

Qy  668 YEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMH 727
Db  709 YEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDDCGEEKLPSCFDYVMH 768

Qy  728 FLTVEFWKVLFACVPPTEYCHGWACFPAVSILILIGMILTAIIGDLASHFGCTIGLKDSVTAVV 787
Db  769 FLTVEFWKVLFAFVPPTEYWNGWACFVVSILMIGLLITAFIGDLASHFGCTIGLKDSVTAVV 828

Qy  788 FVAFGTSVPDTFASRAAALODVYADASIGNVTGSNAVNVFLGIGLAWSIAAAIYWALQGQE 847
Db  829 FVALGTSVPDTFASKVAATODQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQ 888

Qy  848 FHVSAGTLAFSVTLFTIFAFVCISVLLYRRPRHLGGELGGPRGCKLATIWLFVSLWLLYI 907
Db  889 FKVSPGTLAFSVTLFTIFAFINVGLLLYRRPEICGGELGGPRTAKLLTSSLFVLLWLLYI 948

Qy  908 LFATLEAYCYIKGF 921
Db  949 FFSSLEAYCHIKGF 962
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RESULT 11

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ID   Q9WU29      PRELIMINARY;   PRT;   969 AA.
AC   Q9WU29;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Na+/Ca2+-exchanging protein.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RA   Unlap M.T., Bell P.D.;
RT   "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT   Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF109165; AAD23388.1; -.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR004837; NaCa_Exchngr.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx_beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   PRINTS; PR01269; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
SQ   SEQUENCE   969 AA;  108037 MW;  1D64F60730D3C9CF5 CRC64;

Query Match        71.0%;  Score 3406;  DB 11;  Length 969;
Best Local Similarity    68.5%;  Pred. No. 2.3e-240;
Matches  672;  Conservative  105;  Mismatches 128;  Indels  76;  Gaps  11;

Qy    4 LRLQPLTSAFLHFGLVTFVLFL-----------NGLRAEAGGSGDVPSTGQNNESCSGSSSDCK 55
         |||                               ||:||||||||||||||||||||||||||
Db    2 LRLSLPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN------------ETTECTGSYYCK 55
```

```
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cardiac sodium-calcium exchanger.
GN   NCX.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RX   MEDLINE=99447215; PubMed=10516099;
RA   Xue X.H., Hryshko L.V., Nicoll D.A., Philipson K.D., Tibbits G.F.;
RT   "Cloning, expression, and characterization of the trout cardiac
RT   Na(+)/Ca(2+) exchanger.";
RL   Am. J. Physiol. 277:C693-C700(1999).
DR   EMBL; AF175313; AAF06363.1; -.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR004837; NaCa_Exmemb.
DR   InterPro; IPR004836; NaCa_Ex.
DR   InterPro; IPR001299; Na_Ca_Ex; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   Pfam; PF03160; Calx_beta; 2.
DR   PRINTS; PR01259; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
SQ   SEQUENCE   968 AA;  107504 MW;  5F8A92824B26DA36 CRC64;

Query Match             68.8%;  Score 3290.5;  DB 13;  Length 968;
Best Local Similarity   66.2%;
Matches  645;  Conservative  121;  Mismatches  135;  Indels   73;  Gaps   14;
```

```
Qy     10 TSAFLHFGL---VTFVLFLNGLRAEAGGSGDVPSTG------QNNESC-SGSSDCKEGV 58
          ||:|| :||        : ||    |||  ||  |         :|| : |  ::|| ||
Db      6 TSSELFCALQLTVLLAVFSSEIKEVTAGNSN-PSLGTNSSIGNQTNKKCDSVDFECKVGV 64

Qy     59 ILPIWYPENPSLGDKIARVIVFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKIKKPN 118
          ||||| || |:||| |||:||||| ||||||| |||||||||||||||||||:||||||||
Db     65 ILPIWLPENTSFGDKLARATVFVALFYMFLGVSTIADRFMASIEVITSQEREITIKIKKPN 124

Qy    119 GETSTTTIRVWNEIVSNLTLMALGSSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSSAAFNM 178
          ||  ||| || |||||||||||||||||||| |:|:|||| | | ||||| |||||:|||||
Db    125 GEKVTTTVIRIWNEIVSNLTLMALGSSSAPEILSVVEVCGHNFDACDLGPNTIVGSAAFNM 184

Qy    179 FIIIGICVVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWWEGLLTL 238
          |:||| ||:||||| ||:||||||| ||||||||| |||:||||:||| |||||||:||
Db    185 FVIIGFCVSVIPDGEHRKVKHLRVFFVTAAWSIFAYTWLYIILAVISPGIVQVWWEGLVTL 244

Qy    239 FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGD---HPKGIEMDGKMMNS 294
          |||| || :| |||:|||: | | |:||  |:|| ||||||     | | |||||||:||
Db    245 FFFPLCVGMAYVADRRLLYKVMYKRYRAGKRRGVIIETEGEAQIPSKMDIEMDGKMLNS 304

Qy    295 H-FLDGNLVPLEGKEVD-ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSR 351
            | :| : : ||  :| | ||| |||| |:|||:|||: |:|:|||| |:  |||||
Db    305 ESFMDG-AMGFDEKDLDEEEARRENVRILKELKQKIHPEKETEQLIELANYQVLTQQQKSR 363

Qy    352 AFYRIQATRMMTGAGNILKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLEN 410
          |||| |||| :|||||:||:  | ||||| || ||: | |   :|||| :|: :|| ||
Db    364 AFYRCQATRIMTGAGNVLKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGTVIFKPGETEKEIRIDID 423

Qy    411 CGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIID 470
          || | |:||| ||::  |: :: :||| |||| :|:||||| ||: |||| || :  |:|
Db    424 CGTVALNVVRLGGDLTNTVSVEYRTEDGTANAGSDYQFTEGTVVVNPGETEKEIRIDID 483

Qy    471 DDIFEEDEHFFVRLSNVRIEEEQPEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAG 530
          ||||||||||::|:|||::    |   |||     | |||  |:|| |||||:||||||
Db    484 DDIFEEDEHFLVHLSNVKVISEGTGVVQPRA--NHLD-TLAGLGLPCSATVTIFDDDHAG 540

Qy    531 IFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFK 590
          ||| |  ::|:|||||:|||||||||||||:|:||:||:||||||||||||||:| ||| 
Db    541 IFTEEPVMIISESIGMMEVKVLRTSGARGLVVVPYKTMEGTAKGGGEDFEDTHGALEFQ 600

Qy    591 NDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGISDVTDRK--------- 635
          :|:||||:|| :|:||||||||||||||||||||||:: : |:|
Db    601
```

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RESULT 12
US-10-054-680-2
Q9PT19
ID   Q9PT19;    PRELIMINARY;      PRT;   968 AA.
AC   Q9PT19;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
```

```
Qy      2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN------------ETTECTGSYYCK 53

Db     56 EGVILPIWYPENPSLGDKIARVIVFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
Db     54 KGVILPIWEPQDPSFGDKIARATVIFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113
Db    114 KPNGEISTTTIRVWNETVSNLTLMALGSSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 173
Qy    116 KPNGETTKTTVIRIWNEIVSNLTLMALGSSSAPEILPSVIEVCCHNFTAGDLGPSTIVCSSA 175
Db    176 FNMFIIIGICVVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWWEGL 235
Qy    174 FNMFIIIALCVVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVVEWWEGL 233
Db    236 LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG----IEMDGKMM 292
Qy    234 LTFFFFPICVVPAWVADDRLLFYKVYKVKYRYRAGKQRGMIIEHEGDRPASKTEIEMDGKVV 293
Y     293 NSH------FLDGNLVPLEGKEVD------ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS 345
Db    294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKIHPDKEIEQLIELANYQVLS 352
Qy    346 HQQKSRAFYRIQATRMMTGAGNILKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
Db    353 QQQKSRAFYRIQATRLMTGAGNILKRIHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412
Qy    405 YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKRGETQKEF 464
Db    413 YQCLENCGTVALITIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472
Qy    465 SVGIIDDDIFEEDEHFEVRLSNVRIEEEQPEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
Db    473 RVGIIDDDIFEEDENFLVHLSNVRVSSCGVSEDG------ILDSNHVSAIACLGSPNTATITI 528
Qy    524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
Db    529 FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588
Qy    584 YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG------------ 627
Db    589 CGELEFQNDEIVKITIRIFDREEYEKECSFSLVLEEPKWIRGMKALLLNELGGFTLTG 648
Qy    628 -------------ISDVTDRK---LTMEEEAKRIAEMGKPVLGEHPKL 660
Db    649 KKMYGQPVFRKVHARDHPIPSTVISISEEYDDKQPLTSKEEEERIAEMGRPILGEHTKL 708
Qy    661 EVIIEESVEFKTTVDKLLKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720
Db    709 EVIIEESYEFKSTVDKLKIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDCGEEKLPS 768
Qy    721 CFDYVMHFLTVFNKVLFACVPPTEYCHGWACFAVSILLIGMLTAIIGDLASHFGCTIGLK 780
Db    769 CFDYVMHFLTVFNKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLK 828
Qy    781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGIAWSVAAIY 840
Db    829 DSVTAVVFVALGTSVPDIFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIY 888
Qy    841 WALQGQGEPHVSAGTLAFSVTLFFTIFPAFVCISVLLYRRRPHLGGELGGGPRGCKLATTWLFV 900
Db    889 HAANGEQFRKVSPGTLAFSVTLFFIFAFINVGLLLYRRRPEIGGELGGGPRTAKLLTSSLFV 948
Qy    901 SLMLLYILFATLEAYCYIKGF 921
Db    949 LLWLLYIFFSSLEAYCHIKGF 969
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Db  601 NDEIFKSIQINIIDDEEYEKNKNFFLEMGEPQLLE------MSERKAVLLQEIGGFVKTGR 655
        ||||                                     |||||||:|| |:|||
Qy  636 -------------------------LTMEEEEAKRIAEMGKRPVLGEHPKLEVIIEES 667
        ||||:  |||||| :||||||||||||||||
Qy  656 DVYRKVQGRDNPVPATIISLAEEGDEEALSKKEEEERRIAEMGRRTLGEHVKLEVVIEES 715
        :|:|||||| ||||||||||||||
Qy  668 YEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMH 727
        |||| ||||||||||||| || :|||||||| |||| |||||||||||||||||||||
Qy  716 YEFKNTVDKLIKKTNLALLIGTNSWRQQFMEAITVS-SGDDDEDEDCGEEKLPSCFDYVMH 774
        ||||:||||| ||| |:|| :||| |:|||||||| |:|||||||:|||:|||||||||
Qy  728 FLTVFWKVLFACVPPTEYCHGWACFAVSILIIGDLASHFGCTIGLKDSVTAVV 787
        |||||||:||| ||||:| ||||| ||| |:|| ||||||| |||||||||||
Db  775 FLTVFWKLLFAFVPPTDYWNGWACFVVSISMIGLLTAFIGDLASHFGCTVGLKDSVTAVV 834
        ||||||| ||||| |||||||:|:::|:|:|| ||| ||||||||||||:||||||||||
Qy  788 FVAFGTSVPDTFASKAAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQE 847
        |||:|||||||||||||| ||::||||:||||||||||||||||||:|||:|||| |:| |
Db  835 FVALGTSVPDTFASKVAATQDQYADAFIGNVTGSNAVNVFLGIGVAWSIAAIYHNSKGND 894
        ||| |||||||||||:||||||||| ||||||||||||||||||:|||:|||||:| :| :
Qy  848 FHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYI 907
        |:|  |||||||||||||||| | ||||||||:||||||||||| |:||| ||.||| :||
Db  895 FRVDPGTLAFSVTLFTIFAFVAVAVLMYRRRPEIGGELGGPRGPKIATTCLFFSLWLMYI 954
Qy  908 LFATLEAYCYIKGF 921
        |||:|||||:.|||
Db  955 VFSSLEAYCHVKGF 968


RESULT 13
ID  O35157         PRELIMINARY;    PRT;    940 AA.
AC  O35157;
DT  01-JAN-1998 (TrEMBLrel. 05, Created)
DT  01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Sodium-calcium exchanger.
GN  SLC8A1 OR NCX1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/C;
RA  Shi S., Chang B., Brunnert S.R.;
RT  "is the Sodium-Calcium Exchanger a Candidate Gene for Mouse Dystrophic
RT  Cardiac Calcinosis";
RL  Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AF004666; AAB69167.1; -.
DR  MGD; MGI:107956; Slc8a1.
DR  InterPro; IPR004836; Na_Ca_Ex.
DR  InterPro; IPR004837; NaCa_Exmemb.
DR  InterPro; IPR001623; DnaJ_N.
DR  InterPro; IPR003644; Calx_beta.
DR  Pfam; PF01699; Na_Ca_Ex; 2.
DR  Pfam; PF03160; Calx-beta; 2.
DR  Pfam; PF00684; DnaJ_2; 1.
DR  SMART; SM00237; Calx_beta; 2.
DR  PRINTS; PR01259; NACAEXCHNGR.
DR  TIGRFAMS; TIGR00845; caca; 1.
DR  PROSITE; PS50076; DNAJ_2; 1.
DR  PROSITE; PS50074; Calx_beta; 1.
SQ  SEQUENCE  940 AA;  104640 MW;  1E61528CAA62898B CRC64;

Query Match  66.5%;  Score 3191.5;  DB 11;  Length 940;
Best Local Similarity  67.2%;  Pred. No. 1.1e-224;
Matches 631;  Conservative 108;  Mismatches 139;  Indels 61;  Gaps 10;

Qy    4 LRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNESCSGSSSDCKEGVILPIW 63
        |||   | ..:|:||:| |||| ||||||||||||
Db    2 LRLSLPPNVSMGFRLVALVLALLFSHVDHITADTEAETGGNETTECTGSYYCKKGVILPIW 61
Qy   64 YPENPSLGDKIARVIVYFVALIVMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETST 123
        :|| |:|||||||| :||: :|:::|||||||||||||:|||:||||:|:|||||||| :
Db   62 EPQDPSFGDKIARATVFVAMVIMFLGVSIIADRFMSSIEVITSQEKEITIKKPNGETTK 121
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Qy  124 TTIRVWNETVGSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIG 183
        ||:|:||||| |||||||||||||||||| ||||||.| |||||||:|||||||||||||
Db  122 TTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSRIVGSAAFNMFIIIA 181
Qy  184 ICVYVIPDGETRKIKLRVFFITAAWSIFAVIWLYMLAVSPGVVQVWEGLLTFFFPPV 243
        :|||| ||||||||| |||||:|||||||: ||| :| :||||:|||||||||||:
Db  182 LCVYVVPDGETRKIKILRVFFVTAAWSIFATWLYIILSVSSPGVVEVWEGLLTFFFPPI 241
Qy  244 CVLLAWVADKRLLFYXYMHKKYRTKDHKRGIIIEETEGDHPKG---IEMDGKMMNSH---FL 297
        ||: | ||||:|||||||: :||.: || |:||||||| ||:| |.|||||||.||| ||
Db  242 CVVFARWVADRRLLFYXYVYVKYRYRAGKORGMIIEHEGDRPASKTEIEMDGKVVNSHVDNFL 301
Qy  298 DGNLVPLEGKEVD------ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQOKSRAF 353
        || || |  |:|      ::||| :|| ||:|||||||:|| ||:||||| ||||||:||||
Db  302 DGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVILSQQQKSRAF 360
Qy  354 YRIQATRMMTGAGNILKKHAAEQAKRASSMSEVHTDEPE-DFISKYVFFDPCSYQCLENCG 412
        |||||||:|||||||| ||||::|: ||:|:||:::.   |||| |:|| :.|||||||
Db  361 YRIQATRLMTGAGNILKRHAADDQARRAKAVSMHEVNMEMAENDPVSKIFFEQGTYQCLENCG 420
Qy  413 AVLLTVVRKGGDMSKTIMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEEFSVGIIDDD 472
        :| || :|:|||:|:||:|||:|||||:|||:|||||||||||||||:|:|| .|:||||||
Db  421 TVALTIMRRGGDLSTTVFVDDRTEDGTANAGSDYEFTEGTVIFKPGETQKEIRVGIIDDD 480
Qy  473 IFEEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIF 532
        |||| |::|.: ||||:: :.  .   ||:::      :|:::|| .|| || |||||:|||
Db  481 IFEEDENFLVHLSNVRVSSDVSEDGI---LESNHASSIACLGSPSTATIIFDNDHTGIF 537
Qy  533 TFECDIHVSESIGVNEVKVLRTSGARGTVIVPFRTVEGTPAKGGGEDFEDQYGELEFKND 592
        |||  :||||||| :|||||||||||| ||:|.: .||| |:||||||||| | |||:||
Db  538 TFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKITEGGTPARGGGEDFEDTCGVPEFQND 597
Qy  593 ETVKTIRVK-IVDEEYERQENFFIALGEPKNWERG----------- 627
        |:||||.||.| |:|||.: :||: ||||:.:
Db  598 EIVKTISVKVIIDDEEYEKNKT-FIEIGEPRLVEMSEKKALLLNELGGFTLTGKEMYGQP 656
Qy  628 ------ISDVTDRK---LTMEEEEAKRIAEMGKRPVLGEHPKLEVIIEES 667
             :||:|||:   |||||:|:.|:|||||||:|||||||||||||||
Db  657 IFRKVHARDHPIPSTVITISEEYDDKQPLISKEDQERRIAEMGRPILGEHTKLEVIIEES 716
Qy  668 YEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMH 727
        ||||:|||||||||||||||||.|||:||:|||||||| |:::|: |||:|||||||||
Db  717 YEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGERDDDEYGEEKLPSCFDYVMH 776
Qy  728 FLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVV 787
        |||||||||||.||||||:.|||||.|||::||:||| |||||||.||||||||||||||
Db  777 FLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHGCTVGLKDSVTAVV 836
Qy  788 FVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQE 847
        |||:|||||||||||||| ||:||||||||||||||||||||||:|||:|||   | |||
Db  837 FVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAICHAANGEQ 896
Qy  848 FHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELG 886
        |:|  |||||||||||||||| . ||||||||::| :.|
Db  897 FKVSPGTLAFSVTLFTIFAFINVGLLLYRRRPEIGAIFG 935


RESULT 14
Q9EPU8
ID  Q9EPU8         PRELIMINARY;    PRT;    595 AA.
AC  Q9EPU8;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Sodium-calcium exchanger 3 (Fragment).
GN  SLC8A3.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Sokolow S., Herchuelz A., Schurmans S.;
```

```
RT   "Mus musculus mRNA for sodium-calcium exchanger 3 (NCX3), partial
RT   sequence.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF321404; AAG42826.2; -.
DR   MGD; MGI:107976; Slc8a3.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR004837; NaCa_Exmemb.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 1.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
FT   NON_TER        595
FT                  595
SQ   SEQUENCE   595 AA;  66200 MW;  8EF81CBC6EDB7854 CRC64;

Query Match             62.8%;  Score 3012;  DB 11;  Length 595;
Best Local Similarity   97.5%;
  Matches  580;  Conservative    3;  Mismatches   12;  Indels    0;  Gaps    0;
                                     Pred. No. 7.6e-212;

Qy     1  MAWLRLQPLISAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSGSSDCKEGVIL  60
          ||||||||||||||||||||||||||| |||||:||||||:|||||||||||||||||||||
Db     1  MAWLRLQPLISAFLHFGLVTFVLFLNCLRAEAGDSGDVPSAGQONNESCSGSGSSDCKEGVIL  60

Qy    61  PIWYPENPSLGDKIARVIVFAVALIYMFLGVSIIADREVMASIEVITSQEREVTIKKPNGE  120
          |||||||||||||||||||| |||||:||||||||||||:|||||||||||||||||||||
Db    61  PIWYPENPSLGDKIARVIVFAVALIMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE  120

Qy   121  TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI  180

Qy   181  IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF  240

Qy   241  FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN  300

Qy   301  LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQOKSRAFYRIQATR  360
          :||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db   301  FTPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR  360

Qy   361  MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR  420
          ||||||||||:|||||||||:||||||||||||||:||||||||||||||||||||||||
Db   361  MMTGAGNILRKHAAEQAKKTSSMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR  420

Qy   421  KGGDMSKTMVYDKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF  480
          ||||:||||||:|||||||||||||||||||||||||||||||||||||||||:|||||
Db   421  KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF  480

Qy   481  FVRLSNVRIEEEOPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH  540
          |||||||||||||    ||:||||||||||||||||||||||||||||||||||||||||
Db   481  FVRLSNVRIEEEOQLAAGMLPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH  540

Qy   541  VSESIGVMEVKVLRTSGARGTVIVPPRTVEGTAKGGGGEDFEDTYGELEFKNDETV  595
          |||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   541  VSESIGVMEVKVLRTSGARGTVIVPPRTVEGTAKGGGGEDFEDAYGELEFKNDETV  595
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RESULT 15
002196

ID   002196       PRELIMINARY;     PRT;    892 AA.
AC   002196;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Na/Ca exchanger.
GN   NCX-SQ1.
OS   Loligo opalescens (California market squid).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoida;
OC   Myopsida; Loliginidae; Loligo.
OX   NCBI_TaxID=31211;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   He Z., Philipson K.D.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U93214; AAB52920.1; -.
DR   InterPro; IPR003644; Calx_beta.
DR   InterPro; IPR004837; NaCa_Exmemb.
DR   InterPro; IPR004836; Na_Ca_Ex.
DR   Pfam; PF03160; Calx-beta; 2.
DR   Pfam; PF01699; Na_Ca_Ex; 2.
DR   PRINTS; PRO1259; NACAEXCHNGR.
DR   SMART; SM00237; Calx_beta; 2.
DR   TIGRFAMs; TIGR00845; caca; 1.
SQ   SEQUENCE   892 AA;  98517 MW;  ED14O163F2473700 CRC64;

Query Match             52.8%;  Score 2533;  DB 5;  Length 892;
Best Local Similarity   57.1%;
  Matches  516;  Conservative  145;  Mismatches  213;  Indels   30;  Gaps   14;
                                     Pred. No. 1.6e-176;

Qy    23  LFLNGLRAEAGGSGDVPSTGQNNESCSGSGSSD-CKEGVILPIWYP-ENPSLGDKIARVIVY  80
          ||| ||  :   |  |     :::     ||:|| ||| | | |:|  :|||||||:|||:||
Db    14  LFLLGLFFEDFAHASE------DSNDTCTTEAETCRNGLLVPRWNPVGNLSVGDKLARATVY  68

Qy    81  FVALIYMFLGVSIIADREVMASIEVITSQEREVTIKKPNGETSTTIRVWNETVSNLTLMA  140
          ||:| | |||||||||| :|| |||||:|::: |:|||:| |  :||:||||||||||||
Db    69  FVLMFYLFLGVSIIADRFRMAAIEVITSKEKDVVVKKPDGTTVVNVRIWNETVSNLTLMA  128

Qy   141  LGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHL  200
          ||||||||||::||| |::| | : ||||||||||||:||| |||: ||| ||.|:|||
Db   129  LGSSAPEILLSVIEVVGQKFEACQLGPSTIVGSAAFNLFIITAICVTVIPNGEVRTIKHL  188

Qy   201  RVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKY  260
           |||||| : |:|||:|||:|||| | ||| |||||| :||| .|  |||:||||| .||
Db   189  GVFFITATMWSVFAYLWLYFILAVSSYGVVVDVWEGLLTEMFFPATVVTAYIADRLL-NKY  247

Qy   261  MHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRIL  320
           .||| :.|::|:|: : | .  :   . | :::       | ||:: :::   :: ||
Db   248  LSKKYRASKQKGVIVQCEGQODAEEGE--GKSEDGALKEGG-DDVEVREFEQHRKEYIEIL  304

Qy   321  KDLKQKHPEKDLDQLVEMANYYALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKA  380
          :::::||| || :.| ::: . :.:||:||||||||||| ||||:||:|:|  ||:||.|
Db   305  REMRKKNPTLDMKTLEDMAESEAVNRGRKSRAFYRIQATRKLTGSGNIIKK-AKAQAGVA  363

Qy   381  SSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVYDKTEDGSA  440
          .   :| : :::|: :.| |||  : ::|. : .::::| :.|| :||::|||:|||:|
Db   364  QPI--VIDQKPEDEITRVSFDPGHYTVMENVGTFYGTVVTREGGDLTKTLYDKVTEDGTA  421

Qy   441  NAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQP--EEGM  498
          |||:||   |||:| .| ||.|: |:||||||||||||||::|||:.|: :.:   .:|
Db   422  NAGSDYVVAEGTLVFYPMETHKQPFISIIDDDIFEEDEHFYIRLSNLRVGDSNGLFESGQ  481

Qy   499  PPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGA  558
             :.:: ||  ||:| | : |||:||||| ||| : :::.  :|::|| |:|:|:||.|
Db   482  AEA--------KAQLANPFLATVMILDDDHPGIFQIDKEMSVTESSGEVEVRIRTSCA  533

Qy   559  RGTVIVPPRTVEGTAKGGGGEDFEDTYGELEFKNDETVKIRVKIVDEEEYERQENFFIAL  618
          ||.| |||:.|:||| : ||:|:: |:.|| :.|:|| :.||::||:|||||:| ||| |
Db   534  RGCVKVPPHSVDGTAT-YGKDYELVDKDVIFDNDETERFLRVRVVDDEEYEKNETFFIWL  592

Qy   619  GEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKRVLGEHPKLEVIIEESYEFKTTVDKLI  678
           .|  :.. :|| | . :  .. :|.:    ||  || : :| : :||| ||:.|| ||
Db   593  DEPYLVKPTGSSSG---SVVEDDDPVLAELGKPRRGENIKITVHIIESTEFKSVVDDKLL  649

Qy   679  KKTINLALVVGTHSWRDQFMEALTVSAAGDEDEDESGEERLPSCFDYVNHFLTVFWKVLFA  738
          ||  |:|||||:|||:|||:|||||:| |:|:|  |||:||||| ||::||  :||||||
Db   650  KKANLSLVVGTSSWREQFIEALTVNAEGDDDDEGEEEKLPSCMDYIHIFVCLFWKVLFA  709

Qy   739  CVPPTEYCHGWACFAVSILILGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDT  798
          .||||:| .||||| ||:|:||:|||:|||||:.||||||||||:|||| ||:|||||||
Db   710  FVPPTDYWGGWACFTVSIILIGVLTAFIGDLATYFGCTIGLKDAVTAVSFVALGTSVPDT  769

Qy   799  FASKAAAALQDVYADASIGNVTGSNAVNPFLGIGLAWSVAAIYWALQGGEFHVSAGTLAPS  858
          |||||  |||||||||||||||||||||||||||||| |||||||||||| ||||| | |
Db   799  ...
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Db    770  FASKVAAINDKYADSSIGNVTGSNAVNVFLGIGIAWSIAAIYHAANGTVFRVDPGTLAFS  829

Qy    859  VTLFTIFAFVCISVLLYRRPHL-GGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCY  917
           |:|:|||||||||||||  ||: | | |:||:
Db    830  VTIFCVFA-VCTIVLLVCRRHHLVGGELGGPPRCKYITSGILGSFWVSYLILTGLMSYCH  888

Qy    918  IKGF  921
           |.||
Db    889  IPGF  892
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Search completed: November 30, 2002, 12:30:55
Job time : 62.9734 secs